RAW SEQUENCE LISTING

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Application Serial Number: _10/591,484_

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RAW SEQUENCE LISTING   DATE: 09/18/2006
PATENT APPLICATION: US/10/591,484   TIME: 15:21:52

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Output Set: N:\CRF4\09182006\J591484.raw

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 3 <110> APPLICANT: RATAIN, MARK J.
 4        INNOCENTI, FEDERICO
 5        KROETZ, DEANNA L.
 6        UNDEVIA, SAMIR
 7        NYUGEN, TAN
 8        LIU, WANQING
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO THE
11        PHARMACOGENETICS OF DIFFERENT GENE VARIANTS
13 <130> FILE REFERENCE: ARCD:405US
15 <140> CURRENT APPLICATION NUMBER: US/10/591,484
16 <141> CURRENT FILING DATE: 2006-09-01
18 <150> PRIOR APPLICATION NUMBER: PCT/US2005/007410
19 <151> PRIOR FILING DATE: 2005-03-07
21 <150> PRIOR APPLICATION NUMBER: 60/550,268
22 <151> PRIOR FILING DATE: 2004-03-05
24 <160> NUMBER OF SEQ ID NOS: 11
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 4868
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (38)..(4675)
37 <400> SEQUENCE: 1
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40                                              1               5
42 aac tct act ttt tgg aat tcc tca ttc ctg gac agt ccg gag gca gac   103
43 Asn Ser Thr Phe Trp Asn Ser Ser Phe Leu Asp Ser Pro Glu Ala Asp
44              10                  15                  20
46 ctg cca ctt tgt ttt gag caa act gtt ctg gtg tgg att ccc ttg ggc   151
47 Leu Pro Leu Cys Phe Glu Gln Thr Val Leu Val Trp Ile Pro Leu Gly
48          25                  30                  35
50 ttc cta tgg ctc ctg gcc ccc tgg cag ctt ctc cac gtg tat aaa tcc   199
51 Phe Leu Trp Leu Leu Ala Pro Trp Gln Leu Leu His Val Tyr Lys Ser
52          40                  45                  50
54 agg acc aag aga tcc tct acc acc aaa ctc tat ctt gct aag cag gta   247
55 Arg Thr Lys Arg Ser Ser Thr Thr Lys Leu Tyr Leu Ala Lys Gln Val
56  55                  60                  65                  70
58 ttc gtt ggt ttt ctt ctt att cta gca gcc ata gag ctg gcc ctt gta   295
59 Phe Val Gly Phe Leu Leu Ile Leu Ala Ala Ile Glu Leu Ala Leu Val
60          75                  80                  85
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62 ctc aca gaa gac tct gga caa gcc aca gtc cct gct gtt cga tat acc   343
63 Leu Thr Glu Asp Ser Gly Gln Ala Thr Val Pro Ala Val Arg Tyr Thr
64          90                  95                 100
66 aat cca agc ctc tac cta ggc aca tgg ctc ctg gtt ttg ctg atc caa   391
67 Asn Pro Ser Leu Tyr Leu Gly Thr Trp Leu Leu Val Leu Leu Ile Gln
68         105                 110                115
70 tac agc aga caa tgg tgt gta cag aaa aac tcc tgg ttc ctg tcc cta   439
71 Tyr Ser Arg Gln Trp Cys Val Gln Lys Asn Ser Trp Phe Leu Ser Leu
72     120                 125                 130
74 ttc tgg att ctc tcg ata ctc tgt ggc act ttc caa ttt cag act ctg   487
75 Phe Trp Ile Leu Ser Ile Leu Cys Gly Thr Phe Gln Phe Gln Thr Leu
76 135                 140                 145                 150
78 atc cgg aca ctc tta cag ggt gac aat tct aat cta gcc tac tcc tgc   535
79 Ile Arg Thr Leu Leu Gln Gly Asp Asn Ser Asn Leu Ala Tyr Ser Cys
80                 155                 160                 165
82 ctg ttc ttc atc tcc tac gga ttc cag atc ctg atc ctg atc ttt tca   583
83 Leu Phe Phe Ile Ser Tyr Gly Phe Gln Ile Leu Ile Leu Ile Phe Ser
84             170                 175                 180
86 gca ttt tca gaa aat aat gag tca tca aat aat cca tca tcc ata gct   631
87 Ala Phe Ser Glu Asn Asn Glu Ser Ser Asn Asn Pro Ser Ser Ile Ala
88         185                 190                 195
90 tca ttc ctg agt agc att acc tac agc tgg tat gac agc atc att ctg   679
91 Ser Phe Leu Ser Ser Ile Thr Tyr Ser Trp Tyr Asp Ser Ile Ile Leu
92     200                 205                 210
94 aaa ggc tac aag cgt cct ctg aca ctc gag gat gtc tgg gaa gtt gat   727
95 Lys Gly Tyr Lys Arg Pro Leu Thr Leu Glu Asp Val Trp Glu Val Asp
96 215                 220                 225                 230
98 gaa gag atg aaa acc aag aca tta gtg agc aag ttt gaa acg cac atg   775
99 Glu Glu Met Lys Thr Lys Thr Leu Val Ser Lys Phe Glu Thr His Met
100                 235                 240                 245
102 aag aga gag ctg cag aaa gcc agg cgg gca ctc cag aga cgg cag gag   823
103 Lys Arg Glu Leu Gln Lys Ala Arg Arg Ala Leu Gln Arg Arg Gln Glu
104             250                 255                 260
106 aag agc tcc cag cag aac tct gga gcc agg ctg cct ggc ttg aac aag   871
107 Lys Ser Ser Gln Gln Asn Ser Gly Ala Arg Leu Pro Gly Leu Asn Lys
108         265                 270                 275
110 aat cag agt caa agc caa gat gcc ctt gtc ctg gaa gat gtt gaa aag   919
111 Asn Gln Ser Gln Ser Gln Asp Ala Leu Val Leu Glu Asp Val Glu Lys
112     280                 285                 290
114 aaa aaa aag aag tct ggg acc aaa aaa gat gtt cca aaa tcc tgg ttg   967
115 Lys Lys Lys Lys Ser Gly Thr Lys Lys Asp Val Pro Lys Ser Trp Leu
116 295                 300                 305                 310
118 atg aag gct ctg ttc aaa act ttc tac atg gtg ctc ctg aaa tca ttc  1015
119 Met Lys Ala Leu Phe Lys Thr Phe Tyr Met Val Leu Leu Lys Ser Phe
120             315                 320                 325
122 cta ctg aag cta gtg aat gac atc ttc acg ttt gtg agt cct cag ctg  1063
123 Leu Leu Lys Leu Val Asn Asp Ile Phe Thr Phe Val Ser Pro Gln Leu
124         330                 335                 340
126 ctg aaa ttg ctg atc tcc ttt gca agt gac cgt gac aca tat ttg tgg  1111
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127 Leu Lys Leu Leu Ile Ser Phe Ala Ser Asp Arg Asp Thr Tyr Leu Trp
128     345             350             355
130 att gga tat ctc tgt gca atc ctc tta ttc act gcg gct ctc att cag   1159
131 Ile Gly Tyr Leu Cys Ala Ile Leu Leu Phe Thr Ala Ala Leu Ile Gln
132     360             365             370
134 tct ttc tgc ctt cag tgt tat ttc caa ctg tgc ttc aag ctg ggt gta   1207
135 Ser Phe Cys Leu Gln Cys Tyr Phe Gln Leu Cys Phe Lys Leu Gly Val
136 375             380             385             390
138 aaa gta cgg aca gct atc atg gct tct gta tat aag aag gca ttg acc   1255
139 Lys Val Arg Thr Ala Ile Met Ala Ser Val Tyr Lys Lys Ala Leu Thr
140             395             400             405
142 cta tcc aac ttg gcc agg aag gag tac acc gtt gga gaa aca gtg aac   1303
143 Leu Ser Asn Leu Ala Arg Lys Glu Tyr Thr Val Gly Glu Thr Val Asn
144             410             415             420
146 ctg atg tct gtg gat gcc cag aag ctc atg gat gtg acc aac ttc atg   1351
147 Leu Met Ser Val Asp Ala Gln Lys Leu Met Asp Val Thr Asn Phe Met
148     425             430             435
150 cac atg ctg tgg tca agt gtt cta cag att gtc tta tct atc ttc ttc   1399
151 His Met Leu Trp Ser Ser Val Leu Gln Ile Val Leu Ser Ile Phe Phe
152     440             445             450
154 cta tgg aga gag ttg gga ccc tca gtc tta gca ggt gtt ggg gtg atg   1447
155 Leu Trp Arg Glu Leu Gly Pro Ser Val Leu Ala Gly Val Gly Val Met
156 455             460             465             470
158 gtg ctt gta atc cca att aat gcg ata ctg tcc acc aag agt aag acc   1495
159 Val Leu Val Ile Pro Ile Asn Ala Ile Leu Ser Thr Lys Ser Lys Thr
160             475             480             485
162 att cag gtc aaa aat atg aag aat aaa gac aaa cgt tta aag atc atg   1543
163 Ile Gln Val Lys Asn Met Lys Asn Lys Asp Lys Arg Leu Lys Ile Met
164             490             495             500
166 aat gag att ctt agt gga atc aag atc ctg aaa tat ttt gcc tgg gaa   1591
167 Asn Glu Ile Leu Ser Gly Ile Lys Ile Leu Lys Tyr Phe Ala Trp Glu
168     505             510             515
170 cct tca ttc aga gac caa gta caa aac ctc cgg aag aaa gag ctc aag   1639
171 Pro Ser Phe Arg Asp Gln Val Gln Asn Leu Arg Lys Lys Glu Leu Lys
172     520             525             530
174 aac ctg ctg gcc ttt agt caa cta cag tgt gta gta ata ttc gtc ttc   1687
175 Asn Leu Leu Ala Phe Ser Gln Leu Gln Cys Val Val Ile Phe Val Phe
176 535             540             545             550
178 cag tta act cca gtc ctg gta tct gtg gtc aca ttt tct gtt tat gtc   1735
179 Gln Leu Thr Pro Val Leu Val Ser Val Val Thr Phe Ser Val Tyr Val
180             555             560             565
182 ctg gtg gat agc aac aat att ttg gat gca caa aag gcc ttc acc tcc   1783
183 Leu Val Asp Ser Asn Asn Ile Leu Asp Ala Gln Lys Ala Phe Thr Ser
184             570             575             580
186 att acc ctc ttc aat atc ctg cgc ttt ccc ctg agc atg ctt ccc atg   1831
187 Ile Thr Leu Phe Asn Ile Leu Arg Phe Pro Leu Ser Met Leu Pro Met
188     585             590             595
190 atg atc tcc tcc atg ctc cag gcc agt gtt tcc aca gag cgg cta gag   1879
191 Met Ile Ser Ser Met Leu Gln Ala Ser Val Ser Thr Glu Arg Leu Glu
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194 aag tac ttg gga ggg gat gac ttg gac aca tct gcc att cga cat gac   1927
195 Lys Tyr Leu Gly Gly Asp Asp Leu Asp Thr Ser Ala Ile Arg His Asp
196 615                620                625                630
198 tgc aat ttt gac aaa gcc atg cag ttt tct gag gcc tcc ttt acc tgg   1975
199 Cys Asn Phe Asp Lys Ala Met Gln Phe Ser Glu Ala Ser Phe Thr Trp
200                 635                640                    645
202 gaa cat gat tcg gaa gcc aca gtc cga gat gtg aac ctg gac att atg   2023
203 Glu His Asp Ser Glu Ala Thr Val Arg Asp Val Asn Leu Asp Ile Met
204                 650                655                660
206 gca ggc caa ctt gtg gct gtg ata ggc cct gtc ggc tct ggg aaa tcc   2071
207 Ala Gly Gln Leu Val Ala Val Ile Gly Pro Val Gly Ser Gly Lys Ser
208             665                670                675
210 tcc ttg ata tca gcc atg ctg gga gaa atg gaa aat gtc cac ggg cac   2119
211 Ser Leu Ile Ser Ala Met Leu Gly Glu Met Glu Asn Val His Gly His
212     680                685                690
214 atc acc atc aag ggc acc act gcc tat gtc cca cag cag tcc tgg att   2167
215 Ile Thr Ile Lys Gly Thr Thr Ala Tyr Val Pro Gln Gln Ser Trp Ile
216 695                700                705                710
218 cag aat ggc acc ata aag gac aac atc ctt ttt gga aca gag ttt aat   2215
219 Gln Asn Gly Thr Ile Lys Asp Asn Ile Leu Phe Gly Thr Glu Phe Asn
220                 715                720                725
222 gaa aag agg tac cag caa gta ctg gag gcc tgt gct ctc ctc cca gac   2263
223 Glu Lys Arg Tyr Gln Gln Val Leu Glu Ala Cys Ala Leu Leu Pro Asp
224                 730                735                740
226 ttg gaa atg ctg cct gga gga gat ttg gct gag att gga gag aag ggt   2311
227 Leu Glu Met Leu Pro Gly Gly Asp Leu Ala Glu Ile Gly Glu Lys Gly
228     745                750                755
230 ata aat ctt agt ggg ggt cag aag cag cgg atc agc ctg gcc aga gct   2359
231 Ile Asn Leu Ser Gly Gly Gln Lys Gln Arg Ile Ser Leu Ala Arg Ala
232     760                765                770
234 acc tac caa aat tta gac atc tat ctt cta gat gac ccc ctg tct gca   2407
235 Thr Tyr Gln Asn Leu Asp Ile Tyr Leu Leu Asp Asp Pro Leu Ser Ala
236 775                780                785                790
238 gtg gat gct cat gta gga aaa cat att ttt aat aag gtc ttg ggc ccc   2455
239 Val Asp Ala His Val Gly Lys His Ile Phe Asn Lys Val Leu Gly Pro
240                 795                800                805
242 aat ggc ctg ttg aaa ggc aag act cga ctc ttg gtt aca cat agc atg   2503
243 Asn Gly Leu Leu Lys Gly Lys Thr Arg Leu Leu Val Thr His Ser Met
244             810                815                820
246 cac ttt ctt cct caa gtg gat gag att gta gtt ctg ggg aat gga aca   2551
247 His Phe Leu Pro Gln Val Asp Glu Ile Val Val Leu Gly Asn Gly Thr
248             825                830                835
250 att gta gag aaa gga tcc tac agt gct ctc ctg gcc aaa aaa gga gag   2599
251 Ile Val Glu Lys Gly Ser Tyr Ser Ala Leu Leu Ala Lys Lys Gly Glu
252     840                845                850
254 ttt gct aag aat ctg aag aca ttt cta aga cat aca ggc cct gaa gag   2647
255 Phe Ala Lys Asn Leu Lys Thr Phe Leu Arg His Thr Gly Pro Glu Glu
256 855                860                865                870
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259 Glu Ala Thr Val His Asp Gly Ser Glu Glu Glu Asp Asp Asp Tyr Gly
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262 ctg ata tcc agt gtg gaa gag atc ccc gaa gat gca gcc tcc ata acc    2743
263 Leu Ile Ser Ser Val Glu Glu Ile Pro Glu Asp Ala Ala Ser Ile Thr
264                 890                 895                 900
266 atg aca aga gag aac agc ttt cgt cga aca ctt agc cgc agt tat agg    2791
267 Met Arg Arg Glu Asn Ser Phe Arg Arg Thr Leu Ser Arg Ser Ser Arg
268             905                 910                 915
270 tcc aat ggc agg cat ctg aag tcc ctg aga aac tcc ttg aaa act cgg    2839
271 Ser Asn Gly Arg His Leu Lys Ser Leu Arg Asn Ser Leu Lys Thr Arg
272     920                 925                 930
274 aat gtg aat agc ctg aag gaa gac gaa gaa cta gtg aaa gga caa aaa    2887
275 Asn Val Asn Ser Leu Lys Glu Asp Glu Glu Leu Val Lys Gly Gln Lys
276 935                 940                 945                 950
278 cta att aag aag gaa ttc ata gaa act gga aag gtg aag ttc tcc atc    2935
279 Leu Ile Lys Lys Glu Phe Ile Glu Thr Gly Lys Val Lys Phe Ser Ile
280     -   .       955                 960                 965
282 tac ctg gag tac cta caa gca ata gga ttg ttt tcg ata ttc ttc atc    2983
283 Tyr Leu Glu Tyr Leu Gln Ala Ile Gly Leu Phe Ser Ile Phe Phe Ile
284                 970                 975                 980
286 atc ctt gcg ttt gtg atg aat tct gtg gct ttt att gga tcc aac ctc    3031
287 Ile Leu Ala Phe Val Met Asn Ser Val Ala Phe Ile Gly Ser Asn Leu
288         985                 990                 995
290 tgg ctc agt gct tgg acc agt gac tct aaa atc ttc aat agc acc gac    3079
291 Trp Leu Ser Ala Trp Thr Ser Asp Ser Lys Ile Phe Asn Ser Thr Asp
292     1000                1005                1010
294 tat cca gca tct cag agg gac atg aga gtt gga gtc tac gga gct ctg    3127
295 Tyr Pro Ala Ser Gln Arg Asp Met Arg Val Gly Val Tyr Gly Ala Leu
296 1015                1020                1025                1030
298 gga tta gcc caa ggt ata ttt gtg ttc ata gca cat ttc tgg agt gcc    3175
299 Gly Leu Ala Gln Gly Ile Phe Val Phe Ile Ala His Phe Trp Ser Ala
300             1035                1040                1045
302 ttt ggt ttc gtc cat gca tca aat atc ttg cac aag caa ctg ctg aac    3223
303 Phe Gly Phe Val His Ala Ser Asn Ile Leu His Lys Gln Leu Leu Asn
304             1050                1055                1060
306 aat atc ctt cga gca cct atg aga ttt ttt gac aca aca ccc aca ggc    3271
307 Asn Ile Leu Arg Ala Pro Met Arg Phe Phe Asp Thr Thr Pro Thr Gly
308         1065                1070                1075
310 cgg att gtg aac agg ttt gcc ggc gat att tcc aca gtg gat gac acc    3319
311 Arg Ile Val Asn Arg Phe Ala Gly Asp Ile Ser Thr Val Asp Asp Thr
312     1080                1085                1090
314 ctg cct cag tcc ttg cgc agc tgg att aca tgc ttc ctg ggg ata atc    3367
315 Leu Pro Gln Ser Leu Arg Ser Trp Ile Thr Cys Phe Leu Gly Ile Ile
316 1095                1100                1105                1110
318 agc acc ctt gtc atg atc tgc atg gcc act cct gtc ttc acc atc atc    3415
319 Ser Thr Leu Val Met Ile Cys Met Ala Thr Pro Val Phe Thr Ile Ile
320             1115                1120                1125
322 gtc att cct ctt ggc att att tat gta tct gtt cag atg ttt tat gtg    3463
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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number